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Tue Jul 17 13:24:30 2001 [BLASTP 2.1.3 [Apr-1-2001], NCBI]
/home/.../va/Molbio/carpenda/temp1/pl.DNA35639 (390 aa)

Sequences producing High-scoring Segment Pairs:

		Score	Match	Pct	E-val
1	P_AAB53082 ✓ Human angiogenesis-associated protein PRO	2012	390	100	0.0
2	P_AAB80219 ✓ Human PRO246 protein - Homo sapiens.	2012	390	100	0.0
3	P_AAB31207 ✓ human polypeptide PRO246 - Homo sapiens.	2012	390	100	0.0
4	P_AAB68599 ✓ PRO246 - Homo sapiens.	2012	390	100	0.0
5	P_AAB88358 ✓ Human membrane or secretory protein clone	2012	390	100	0.0
6	P_AAY94999 ✓ Human secreted protein vc51_1, SEQ ID NO:	2012	390	100	0.0
7	P_AAY88574 ✓ Human PRO246 amino acid sequence - Homo s	2012	390	100	0.0
8	P_AAY05286 ✓ EGF-like homologue PRO246 - Homo sapiens.	2012	390	100	0.0
9	P_AAY13351 ✓ protein PRO246 - Homo sapiens.	2012	390	100	0.0
10	P_AAY27096 ✓ Human viral receptor protein (ACVRP) - Ho	2012	390	100	0.0
11	P_AAB90818 ✓ Human shear stress-response protein SEQ I	2004	389	100	0.0
12	P_AAY76303 ✓ Fragment of human secreted protein encode	2003	388	100	0.0
13	P_AAB65832 Human INTERCEPT 258 SEQ ID NO: 28 - Homo	1734	341	94	0.0
14	P_AAB65906 Human secreted protein related protein SE	1732	340	94	0.0
15	P_AAB65907 Human secreted protein related protein SE	1730	340	94	0.0
16	P_AAB65905 Human secreted protein related protein SE	1730	340	94	0.0
17	P_AAB65904 Human secreted protein related protein SE	1730	340	94	0.0

>1 P_AAB53082 Human angiogenesis-associated protein PRO246, SEQ ID NO:96 - Homo sapiens. (390 aa) [1 seg]

Score = 2012 (779 bits), Expect = 0.0

Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

DNA35639	1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

P_AAB53082	1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639	61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD

P_AAB53082	61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD

DNA35639	121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

P_AAB53082	121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

DNA35639	181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTAAQCNVTLE

P_AAB53082	181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTAAQCNVTLE

DNA35639	241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAIAAPRTLWPKS

P_AAB53082	241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAIAAPRTLWPKS

DNA35639	301 SDTISKNGTLSSVTSARALRPPHGPRLPGALTPTPSLSSQALPSPLPTTDGAHPQPISP

P_AAB53082	301 SDTISKNGTLSSVTSARALRPPHGPRLPGALTPTPSLSSQALPSPLPTTDGAHPQPISP

DNA35639	361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

P_AAB53082	361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>2 P_AAB80219 Human PRO246 protein - Homo sapiens. (390 aa) [1 seg]

BLAST RESULTS B-1

Score = 2012 (779 bits), Expect = 0.0
 Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

DNA35639	1	MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV *****
P_AAB80219	1	MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV *****
DNA35639	61	SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD *****
P_AAB80219	61	SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD *****
DNA35639	121	SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK *****
P_AAB80219	121	SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK *****
DNA35639	181	PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE *****
P_AAB80219	181	PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE *****
DNA35639	241	VSTGPGAAVVAGAVVGTLVGLLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS *****
P_AAB80219	241	VSTGPGAAVVAGAVVGTLVGLLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS *****
DNA35639	301	SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPLRLPTTDGAHPQPISP *****
P_AAB80219	301	SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPLRLPTTDGAHPQPISP *****
DNA35639	361	IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV *****
P_AAB80219	361	IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV *****

>3 P_AAB31207 human polypeptide PRO246'- Homo sapiens. (390 aa) [1 seg]
 Score = 2012 (779 bits), Expect = 0.0
 Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

DNA35639	1	MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV *****
P_AAB31207	1	MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV *****
DNA35639	61	SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD *****
P_AAB31207	61	SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD *****
DNA35639	121	SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK *****
P_AAB31207	121	SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK *****
DNA35639	181	PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE *****
P_AAB31207	181	PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE *****
DNA35639	241	VSTGPGAAVVAGAVVGTLVGLLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS *****
P_AAB31207	241	VSTGPGAAVVAGAVVGTLVGLLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS *****
DNA35639	301	SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPLRLPTTDGAHPQPISP *****

P_AAB31207 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPLPTTDGAHPQPISP

DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

P_AAB31207 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>4 P_AAB68599 PRO246 - Homo sapiens. (390 aa) [1 seg]
Score = 2012 (779 bits), Expect = 0.0
Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

P_AAB68599 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

P_AAB68599 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

P_AAB68599 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

P_AAB68599 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAEDAIAPRTL PWPKS

P_AAB68599 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAEDAIAPRTL PWPKS

DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPLPTTDGAHPQPISP

P_AAB68599 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPLPTTDGAHPQPISP

DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

P_AAB68599 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>5 P_AAB88358 Human membrane or secretory protein clone PSEC0086 - Homo (390 aa) [1 seg]
Score = 2012 (779 bits), Expect = 0.0
Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

P_AAB88358 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

P_AAB88358 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

P_AAB88358 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

P_AAB88358 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKAIA PRTLPWPKS

P_AAB88358 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKAIA PRTLPWPKS

DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPRLPTTDGAHPQPISP

P_AAB88358 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPRLPTTDGAHPQPISP

DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

P_AAB88358 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>6 P_AAY94999 Human secreted protein vc51_1, SEQ ID NO:38 - Homo sapiens. (390 aa) [1 seg]
Score = 2012 (779 bits), Expect = 0.0
Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

P_AAY94999 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

P_AAY94999 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQSPRSK

P_AAY94999 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQSPRSK

DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

P_AAY94999 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKAIA PRTLPWPKS

P_AAY94999 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKAIA PRTLPWPKS

DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPRLPTTDGAHPQPISP

P_AAY94999 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPRLPTTDGAHPQPISP

DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

P_AAY94999 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>7 P_AAY88574 Human PRO246 amino acid sequence - Homo sapiens. (390 aa) [1 seg]
Score = 2012 (779 bits), Expect = 0.0
Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

P_AAY88574 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

P_AAY88574 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD

DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

P_AAY88574 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

P_AAY88574 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS

P_AAY88574 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS

DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPRLPTTDGAHPQPISP

P_AAY88574 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPRLPTTDGAHPQPISP

DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

P_AAY88574 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>8 P_AAY05286 EGF-like homologue PRO246 - Homo sapiens. (390 aa) [1 seg]
Score = 2012 (779 bits), Expect = 0.0
Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

DNA35639 1 MISLPGPLVTNLLRFLFLGLSLAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

P_AAY05286 1 MISLPGPLVTNLLRFLFLGLSLAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD

P_AAY05286 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD

DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

P_AAY05286 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

P_AAY05286 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS

P_AAY05286 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS

DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPRLPTTDGAHPQPISP

P_AAY05286 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPRLPTTDGAHPQPISP

DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

P_AAY05286 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>9 P_AAY13351 protein PRO246 - Homo sapiens. (390 aa) [1 seg]
Score = 2012 (779 bits), Expect = 0.0
Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

 P_AAY13351 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

 DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

 P_AAY13351 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

 DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 P_AAY13351 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 DNA35639 181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

 P_AAY13351 181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

 DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKAIAAPRTLPWPKS

 P_AAY13351 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKAIAAPRTLPWPKS

 DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPrPGALTPTPSLSSQALPSPLPTTDGAHPQPISP

 P_AAY13351 301 SDTISKNGTLSSVTSARALRPPHGPPrPGALTPTPSLSSQALPSPLPTTDGAHPQPISP

 DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

 P_AAY13351 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>10 P_AAY27096 Human viral receptor protein (ACVRP) - Homo sapiens. (390 aa) [1 seg]

Score = 2012 (779 bits), Expect = 0.0

Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

 P_AAY27096 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

 DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

 P_AAY27096 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

 DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 P_AAY27096 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 DNA35639 181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

 P_AAY27096 181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

 DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKAIAAPRTLPWPKS

 P_AAY27096 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKAIAAPRTLPWPKS

 DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPrPGALTPTPSLSSQALPSPLPTTDGAHPQPISP

 P_AAY27096 301 SDTISKNGTLSSVTSARALRPPHGPPrPGALTPTPSLSSQALPSPLPTTDGAHPQPISP

DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

 P_AAY27096 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>11 P_AAB90818 Human shear stress-response protein SEQ ID NO: 144 - Homo (390 aa) [1 seg]

Score = 2004 (776 bits), Expect = 0.0
 Identities = 389/390 (99%), Positives = 389/390 (99%), at 1,1-390, 390

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

 P_AAB90818 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

 DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD

 P_AAB90818 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD

 DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 P_AAB90818 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

 P_AAB90818 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

 DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAIA PRTL PWPKS

 P_AAB90818 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAIA PRTL PWPKS

 DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPRLPTTDGAHPQPISP

 P_AAB90818 301 SDTISKNGTLSSVTSARALWPPHGPPRGALTPPSLSSQALPSPRLPTTDGAHPQPISP

 DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

 P_AAB90818 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>12 P_AAY76303 Fragment of human secreted protein encoded by gene 29 - Homo (389 aa) [1 seg]

Score = 2003 (776 bits), Expect = 0.0
 Identities = 388/389 (99%), Positives = 389/389 (99%), at 1,1-389, 389

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

 P_AAY76303 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

 DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD

 P_AAY76303 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD

 DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 P_AAY76303 121 SGPYSCSVNVQNKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

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P_AAY76303 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIA PRTLPWPKS

P_AAY76303 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIA PRTLPWPKS

DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP

P_AAY76303 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP

DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSL

P_AAY76303 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSL

>13 P_AAB65832 Human INTERCEPT 258 SEQ ID NO: 28 - Homo sapiens. (370 aa) [1 seg]

Score = 1734 (672 bits), Expect = 0.0

Identities = 341/362 (94%), Positives = 344/362 (94%), Gaps = 7/362 (1%), at 1,1-355,362

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

P_AAB65832 1 MISLPGPLVTNLXRFLLGLSALAPPSRAQLQLHLPANRLQAVEEGESGASAWYTLHREV

DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKD

P_AAB65832 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRVEGLQEKD

DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

P_AAB65832 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

P_AAB65832 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIA PRTLPWPKS

P_AAB65832 241 VSTGPGAAVVAEAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIA PRTLPWPKS

DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPR-----LPTTDGA

P_AAB65832 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRHAHDRWGPPSTNIP

DNA35639 354 HP

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P_AAB65832 361 HP

>14 P_AAB65906 Human secreted protein related protein SEQ ID NO: 138 - Homo (370 aa) [1 seg]

Score = 1732 (671 bits), Expect = 0.0

Identities = 340/362 (93%), Positives = 344/362 (94%), Gaps = 7/362 (1%), at 1,1-355,362

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

P_AAB65906 1 MISLPGPLVTNLXRFLLGLSALAPPSRAQLQLHLPANRLQAVEEGESGASAWYTLHREV

DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

 P_AAB65906 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRVEGLQEKD

 DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 P_AAB65906 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRIQGVPHVGANVTLSCQSPRSK

 DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

 P_AAB65906 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

 DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPKS

 P_AAB65906 241 VSTGPGAAVVAEAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPKS

 DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPSLSSQALPSPR-----LPTTDGA

 P_AAB65906 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPSLSSQALPSPRHAHDRWGPPSTNIP

 DNA35639 354 HP
 **
 P_AAB65906 361 HP

>15 P_AAB65907 Human secreted protein related protein SEQ ID NO: 140 - Homo (370
 aa) [1 seg]
 Score = 1730 (671 bits), Expect = 0.0
 Identities = 340/362 (93%), Positives = 343/362 (93%), Gaps = 7/362 (1%), at
 1,1-355,362

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

 P_AAB65907 1 MISLPGPLVTNLXRFFLGLSALAPPSRAQLQLHLPANRLQAVEEGESGASAWYTLHREV

 DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

 P_AAB65907 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRVEGLQEKD

 DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 P_AAB65907 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

 P_AAB65907 181 PVVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

 DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPKS

 P_AAB65907 241 VSTGPGAAVVAEAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPKS

 DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPSLSSQALPSPR-----LPTTDGA

 P_AAB65907 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPSLSSQALPSPRHAHDRWGPPSTNIP

 DNA35639 354 HP
 **

DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS

P_AAB65904 241 VSTGPGAAVVAEAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS

DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPR-----LPTTDGA
***** *.
P_AAB65904 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRHAHDRWGPPSTNIP

DNA35639 354 HP
**
P_AAB65904 361 HP